

**Supplemental Figure 1 Distribution of BAC clone insert lengths.** Paired BAC end sequences aligned within the same genomic sequencing scaffold, providing an estimate of their physical size. Apparent insert lengths ranged from 1 kb to 107 kb, distributed bimodally, with 79% of the clones having mean length of  $70 \pm 10$  kb and 21% of clones having a shorter mean length of  $17 \pm 10$  kb (parameters estimated by Maximum Likelihood of a mixture of two Normal distributions, predicted distribution shown by dotted line). This length distribution allows reliable estimates of physical gap sizes to be calculated adjacent scaffold spanned by BAC clones.

